

METHOD, COMPOSITIONS AND KIT FOR DETECTION OF MICROORGANISMS AND
BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID POLYMERS

This application is a continuation-in-part of pending US Patent Applications Nos. 09/009,483 filed January 20, 1998, 08/640,672 filed May 1, 1996, now US Patent No. 5,789,168, 08/684,498 filed July 19, 1996, now US Patent No. 5,830,657, and 08/807,138 filed February 27, 1997, now US Patent No. 5,888,736, and of International Patent Application No. PCT/US97/07134 filed April 29, 1997 designating the United States, and published as International Publication No. WO 97/41259 on November 6, 1997, all of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

This application relates to a method for detection and identification of microorganisms, including in particular pathogenic microorganisms, and to compositions and kits useful in practicing the method. The invention can be applied to detection of viruses, including HIV and hepatitis, bacteria, including *Chlamydia*, fungi, including *Cryptococcus neoformans* and protozoa, including *Trypanosoma cruzi*. This application also relates to DNA sequencing reactions, and in particular to improved bi-directional sequencing reaction protocols making use of thermally stable polymerase enzymes.

Detection of the presence of pathogenic microorganisms through DNA-based technology is emerging as an important tool in the diagnosis of many diseases. For example, diagnosis of *Chlamydia trachomatis* infections, the most common bacterial sexually transmitted disease in North America, is shifting from traditional methods such as culture, enzyme immunoassay (EIA) and direct fluorescent antibodies (DFA) to DNA-hybridization diagnostics. Roche Diagnostic Systems, Inc. (Nutley, NJ) manufactures Amplicor™, a test which detects *C. trachomatis* and *Neisseria gonorrhoeae* by the hybridization of a pathogen specific probe to PCR amplified products, detectable by a color

change/optical density technique. Abbott Laboratories (Abbott Park, IL) makes UriProbe, also a test for *C. trachomatis* and *N. gonorrhoeae*, which relies on the ligase chain reaction (LCR). The LCR method, described in Patent Applications WO 9320227, WO 9300447, WO 9408047, WO 9403636, EP 477 972 uses thermostable ligase enzyme to ligate two DNA probes which hybridize in ligatable juxtaposition on a template DNA strand, thus generating a detectable ligated DNA fragment only if the template DNA is present. A multiplex PCR assay for *C. trachomatis* has also been described in Mahony et al., *J. Clin. Microbiol.* 33: 3049-3053 (1995).

The ideal DNA sequencing procedure for use in a diagnostic environment would have the following characteristics: (1) it would be able to utilize a DNA-containing sample which had been subjected to only minimal pretreatment to make the DNA accessible for sequencing; (2) it would require combining this sample with only a single reaction mixture, thus reducing risk of error and contamination, and increasing the ease with which the procedure can be automated; and (3) it would require a short amount of time to perform the sequence determination, thus decreasing the marginal costs in terms of equipment and labor for performing the test.

A wide variety of infectious pathogens that can be detected by DNA-based methods are listed in *Diagnostic Molecular Microbiology*, Persing et al., eds. American Society for Microbiology, Washington D.C. (1993). This text details diagnostic tests for bacteria, virus, fungi, and protozoa. Diagnostic tests are also proposed for identifying the presence of drug resistance genes or toxin genes.

Although these tests are generally effective for identifying an infectious disease-causing organism if present, they do not routinely provide information concerning the specific serotype, variant or form of the infecting organism. Depending on the organism in question, this information can be significant in determining the likely course of the infection, for determining the most appropriate therapeutic approach and for epidemiological purposes. Furthermore, the previously known assays involve several steps and are therefore more

5 susceptible to systematic error than would be a test with fewer steps. Thus, there remains a need for a simple test format which is generally applicable to the detection of microorganisms, including infectious disease-causing microorganisms, and particularly for a simple test which provides an indication of the specific nature, e.g., the serotype, of the organism. It is an object of the present invention to provide such a test.

It is an object of the present invention to provide reagent combinations useful in performing tests for infectious disease-causing microorganisms, including *Chlamydia* human papilloma virus(HPV) and HIV.

10 It is a further object of the present invention to provide kits useful in performing tests for infectious disease-causing microorganisms, including *Chlamydia*, HPV and HIV.

It is an additional object of the present invention to provide an improved method for bi-directional sequencing of DNA samples which is well-suited for use in the diagnostic environment and for automation.

15 It is an additional object of the invention to provide a method for bi-directional sequencing of DNA which utilizes a DNA-containing sample which has been subjected to only minimal pretreatment to make the DNA accessible for sequencing.

20 It is still a further object of the invention to provide a method for bi-directional sequencing of DNA which requires combining a complex DNA-containing sample with only a single reaction mixture, thus reducing risk of error and contamination, and increasing the ease with which the procedure can be automated.

SUMMARY OF THE INVENTION

25 The present invention provides a method for the evaluation of a sample for the presence of a target microorganism which can be performed directly on a natural abundance DNA preparation obtained from the sample in a single reaction vessel. The method of the invention comprises the steps of:

1 (a) combining the natural abundance DNA preparation with first and second
primers, a nucleotide triphosphate feedstock mixture, a chain-terminating nucleotide
triphosphate and a thermally stable polymerase enzyme which incorporates
dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4
5 times the rate of incorporation of deoxynucleotides to form a reaction mixture, said first and
second primers binding to the sense and antisense strands of the DNA of the target
microorganism, respectively, and flanking a selected region within the genome of the target
microorganism;

10 (b) exposing the reaction mixture to a plurality of temperature cycles each of
which includes at least a high temperature denaturation phase and a lower temperature
extension phase, thereby producing a plurality of species of terminated fragments if DNA
from the target microorganism is present in the sample, each species of terminated fragment
corresponding to a different incorporation position for the chain-terminating nucleotide
triphosphate in the DNA of the target microorganism; and

15 (c) evaluating the terminated fragments produced to determine the
incorporation positions of the chain-terminating nucleotide triphosphate. Based on the
incorporation positions, not only the presence but also the specific nature, e.g. the serotype,
of any target microorganism present can be determined.

20 The present invention also provides a composition comprising a mixture of four
deoxynucleotide triphosphates and at least one dideoxynucleotide triphosphate
corresponding to one of the four deoxynucleotide triphosphates, wherein the
dideoxynucleotide triphosphate is present in a mole ratio to the corresponding
deoxynucleotide triphosphate of from 1:50 to 1:500, said composition further comprising a
thermally stable polymerase enzyme which incorporates dideoxynucleotides into an extending
25 nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of
deoxynucleotides.

Also provided is a kit for detection of a target microorganism comprising, in packaged combination, the above composition and a pair of primers which bind to the sense and antisense strands, respectively, and flank a selected region within the genome target microorganism.

5 The present invention also provides a method for bi-directional sequencing a region of interest in a DNA sample. The method can be carried out using a single set of reagents which is added to a minimally-treated sample to produce useful sequencing results.

DETAILED DESCRIPTION OF THE INVENTION

10 The compositions and kits of the present invention can be employed in a bi-directional DNA sequencing method in many contexts including: (1) detection of mutations, particularly mutations of medical significance, in samples derived from a human patient, animal, plant or microorganism; (2) determination of HLA type ancillary to transplant procedures; (3) detection and identification of microorganisms, particularly pathogenic microorganisms, in a sample; and (4) in-situ sequencing reactions to produce sequencing fragments within a histological specimen which are then removed from a selected location on the tissue preparation and loaded onto a gel for sequence analysis. This latter approach is particularly useful for evaluation of archived samples in retrospective studies where the outcome of a disease condition is known, but the potentially causative mutation is not. This method can be used
15 with labeled primers for single base sequencing (or multiple-base sequencing using multiple tissue samples).

20 In the context of detecting and identifying microorganisms, the invention provides a novel approach to the evaluation of a sample for the presence of a target microorganism and for the identification of the specific nature of any organism found to be present. The target
25 microorganism may be virus, bacteria, fungi or protozoa. Specific non-limiting examples of microorganisms to which the invention can be suitably applied include bacteria such as *Mycobacteria tuberculosis*, *Rickettsia rickettsii*, *Ehrlichia chaffeensis*, *Borrelia burgdorferi*,

Yersinia pestis, *Treponema pallidum*, *Chlamydia trachomatis*, *Chlamydia pneumoniae*,
Mycoplasma pneumoniae, *Mycoplasma sp.*, *Legionella pneumophila*, *Legionella dumoffii*,
Mycoplasma fermentans, *Ehrlichia sp.*, *Haemophilus influenzae*, *Neisseria meningitidis*,
Streptococcus pneumoniae, *S. agalactiae*, and *Listeria monocytogenes*; viruses such as
Human Immunodeficiency Virus Type 1 (HIV-1), Human T-Cell Lymphotropic Virus Type 1
(HTLV-1), Hepatitis B Virus (HBV), Hepatitis C Virus (HCV), Herpes Simplex, Herpesvirus 6,
Herpesvirus 7, Epstein-Barr Virus, Cytomegalovirus, Varicella-Zoster Virus, JC Virus,
Parvovirus B19, Influenza A, B and C, Rotavirus, Human Adenovirus, Rubella Virus, Human
Enteroviruses, Genital Human Papillomavirus (HPV), and Hantavirus; fungi such as
Cryptococcus neoformans, *Pneumocystis carinii*, *Histoplasma capsulatum*, *Blastomyces*
dermatitidis, *Coccidioides immitis*, and *Trichophyton rubrum*; and protozoa such as
Trypanosoma cruzi, *Leishmania sp.*, *Plasmodium*, *Entamoeba histolytica*, *Babesia microti*,
Giardia lamblia, *Cyclospora sp.* and *Eimeria sp.* The method of the invention may also be
used for *Cryptosporidium* oocyst detection; for identification of bacterial toxin genes, such as
the toxin genes from *Vibrio cholerae* 01, enterotoxigenic *Escherichia coli*, *Shigella sp.*,
enteroinvasive *E. coli*, *Helicobacter pylori* (formerly *Campylobacter pylori*), toxigenic
Clostridium difficile, *Staphylococcus aureus*, and *Streptococcus pyogenes* exotoxins; and
for identification of anti-microbial resistance loci such as rifampin resistance mutations in
Mycobacterium tuberculosis and *M. leprae*; HIV Drug Resistance, *erm* Erythromycin
Resistance Genes, methicillin--resistance genes in *Staphylococcus*, Penicillinase-Producing
genes in *Neisseria gonorrhoeae*, genes encoding aminoglycoside-modifying enzymes,
genes encoding an extended spectrum of Beta-Lactamases, fluoroquinolone and isoniazid
resistance mutations in *Mycobacterium tuberculosis*, and genes encoding
vancomycin resistance in Enterococci.

The method of detecting and identifying the presence of a target microorganism may
utilize bi-directional DNA sequencing, in which a natural abundance DNA-containing sample

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suspected to contain the target microorganism is combined in a reaction mixture with (1) first and second primers that hybridize with the sense and antisense strands of the DNA of the target microorganism, respectively, and flank a selected region within the genome of the target microorganism, (2) a nucleotide triphosphate feedstock mixture, (3) at least one chain-terminating nucleotide triphosphate and (4) a polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides to form a reaction mixture. This reaction mixture is processed through a plurality of thermal cycles. Each thermal cycle includes at least an extension step which is performed at a temperature of around 68 to 75 °C and a denaturation step performed at a temperature of around 90 to 98 °C. In addition, the thermal cycles may include a separate annealing step performed at a temperature of 50 to 70 °C.

During each cycle, the primers each anneal to the respective strand of any target DNA present in the sample, and primer chain extension using the polymerase enzymes and the nucleotide triphosphate feedstocks proceeds until terminated by incorporation of a chain-terminating nucleotide triphosphate. This results in the production of sequencing fragments comparable to those generated in a conventional sequencing reaction. Analysis of these fragments provides information concerning the sequence of the selected region of the target DNA, and thus of the serotype of the target microorganism. Those extension products which are not terminated prior to reaching the region complementary to the other primer can serve as template for generation of sequencing fragments in later cycles, although this generally occurs to a very small extent. This method also provides for simultaneously determining the positions of a selected nucleotide base in a target region of both strands of a denatured duplex nucleic acid polymer. The method of the invention differs from the prior art, because the first and second oligonucleotide primers are each labeled with different, spectroscopically-distinguishable fluorescent labels. The method therefore obtains information about both DNA strands simultaneously while providing improved sensitivity as a

result of the non-linear increase in the amount of DNA which results from the production of additional templates molecules from unterminated fragments.

Among the advantages of the present invention is the ability to perform an evaluation directly on a "natural abundance" DNA sample. The nature of the initial sample will depend on the nature of the target microorganism. For example, in the case of *Chlamydia*, the initial sample employed in the present invention is suitably a urine sample, genital scraping or genital swab taken from a human patient, although other samples which are suspected of containing *Chlamydia* can also be tested using the method of the invention. Similarly, to test for HIV infection, the preferred sample is a blood sample.

As used herein a "natural abundance sample" is a sample which has been treated to make DNA in the sample accessible for hybridization with oligonucleotide primers, for example by lysis, centrifugation to remove cellular debris and proteolytic digestion to expose the DNA, but which has not been subjected to a preferential purification or amplification step to increase the amount of target DNA relative to non-target DNA present in the initial sample. The term "natural abundance" does not, however, require the presence of all the DNA from the original sample. Thus, a complex sample containing just nuclear DNA, or just mitochondrial DNA or some subfraction of nuclear or mitochondrial DNA obtained by isolation from a tissue sample but not subjected to preferential amplification would be a "natural abundance" sample within the meaning of that term in the specification and claims of this application. The term "natural abundance" would also include a DNA sample prepared by conversion, for example by reverse transcription, of a total mRNA preparation or the genome of an RNA virus to cDNA; DNA isolated from an individual bacterial colony growing on a plate or from an enriched bacterial culture; and a viral DNA preparation where substantially the entire viral genome is isolated. The term "natural abundance" does not encompass a sample in which the isolated DNA is not a complex combination of DNA molecules, and thus would not encompass, for example, a purified plasmid preparation containing only a single species of plasmid.

Natural abundance samples of mammalian DNA can be prepared from fluid samples, e.g., blood or urine or tissue samples by any of a number of techniques, including lysis, centrifugation to remove cellular debris and proteolytic digestion to expose the DNA; salt precipitation or standard SDS-proteinase K-phenol extraction. Natural abundance samples can also be prepared using kits, for example the Gentra PURE GENE DNA Isolation Kit.

Primers used in the method of the present invention can be any pair of primers which hybridize with the sense and antisense strands DNA of the target microorganism flanking a selected region of diagnostic relevance, and which do not both hybridize to neighboring locations in human DNA or other microbial DNA potentially found in the sample. As used herein, the term "flanking" will be understood to mean the positioning of primers at the 5'-ends of the selected region on each DNA strand, such that extension of the primers leads to replication of the region between the primers. The primers are preferably selected such that the primer pair flanks a region that is about 500 bp or less, although primers spanning larger regions of DNA can be utilized with adjustments to the sequencing mixture (generally an increase in the relative amount of deoxynucleotide triphosphates) to increase the amount of longer sequencing fragments produced.

Primers can be selected to hybridize with highly conserved regions which are the same in all variants of the target microorganism or can be prepared as degenerate primers to take known sequence variations at the primer site into account. Thus, the first and second primers of the invention may each be a discrete oligonucleotide species, or may be a set of oligonucleotide primers with similar but not identical sequences. Primers can also be selected to bind to the sense and antisense strands of DNA flanking a region of the genome of the target microorganism which is constant across all known variants and forms of the microorganism, in which case the method of the invention would provide detection but not any specific qualitative characterization of the microorganisms, i.e., such primers could not provide discrimination between subspecies, serovars, strains, sub-types, biovars, variants, serotypes or between closely related species of the target microorganism. An example of

such a primer pair is a primer pair that binds to the cryptic plasmid of *C. trachomatis* which is recognized as a suitably specific target sequence or detection purposes, but which is not known to vary from strain to strain. Preferably, however, the primers employed will flank a region of the target genome which is variable in sequence depending on the serotype of the organism. Thus, for *C. trachomatis* primers which flank portions of the omp1 gene are preferred. Similarly, in the case of HIV detection, primers flanking known mutation sites in the HIV protease gene or reverse transcriptase gene produce fragments which permit both detection of HIV and the identification of the HIV variant present in the sample. Primers MY09 and MY11 (See example 10) give sequence information for most relevant types of human papilloma virus (HPV) but not other viruses.

In an alternative embodiment, primer pairs are selected which, when treated under the conditions of the invention, give sequence information from a much wider variety of organisms. This is the case with eubacterial "universal" primers such as 91E and 13B listed in Appendix I which can be used to obtain sequence data from the 16S rDNA gene of many bacteria. These primers are useful for identifying which bacterium is present in a septic blood culture, or any other pure but unknown culture. Patient samples which contain a broad range of bacteria will give a complex result, consisting of many overlapping sequences when tested with these primers. The complex result may, in some cases, provide useful information about the bacteria present. However, in the normal course, it is advantageous to separate out the species, i.e. by plating them out first. In this case, individual pure colonies can be selected and identified.

In still another embodiment, the primer pairs are selected to determine whether a specific gene is present in the patient sample. The gene can be a toxin gene, a virulence gene, an anti-biotic resistance gene or a specific mutation which confers drug resistance or the like. Such a test can determine if a micro-organism is present and if it carries the gene at the same time.

Primers for other microorganisms can be derived from known sequence information. Appendix I lists a collection of suitable primer pairs for various other microorganisms which are taken from Persing et al., *supra*.

One or both of the primers may be labeled with a detectable label at the 5'-end thereof, particularly a fluorescent label such as fluorescein or a cyanine dye such as Cy 5.5. If labels are used on both primers, the labels selected should be spectroscopically-distinct, i.e., they should have either a different excitation spectrum or a different emission spectrum such that one primer can be distinguished from the other. When both primers are labeled with different detectable labels, the sequence of both strands of the sample can be determined in a single reaction.

The nucleotide triphosphate feedstock mixture is a standard mixture of the four conventional bases (A, C, G and T) in a buffer suitable for template-dependent primer extension with the enzyme employed. As will be appreciated by persons skilled in the art, the specific concentrations of the nucleotide triphosphates and the nature of the buffer will vary depending on the enzyme employed. Standard buffers and reagent concentrations for various known polymerase enzymes may be employed in the invention.

The reaction mixture used in the present invention also includes at least one type of chain-terminating nucleotide triphosphate. Separate reactions for the four different types of bases may be run either concurrently or successively. Running all four bases concurrently comports with conventional sequencing practice. However, a preferred embodiment of the present invention combines the single vessel methodology of this application with "single track sequencing" which is described in commonly assigned US Patent No. 5,835,189. In single track sequencing, the determination of the positions of only one (or in any event less than 4) nucleotide(s) of a target sequence is frequently sufficient to establish the presence of and determine the qualitative nature of a target microorganism by providing a finger-print or bar-code of the target sequence that may be sufficient to distinguish it from all other known varieties of the sequence. Throughput is increased by reducing the number of reactions and

electrophoresis runs required to identify a sequence. By selection of the order of bases tested, and intermediate analysis, it may be unnecessary to run all four bases to determine the presence and specific qualitative nature of any target microorganism present in the sample.

5 The polymerase enzyme used in the invention is a thermostable polymerase enzyme which incorporates dideoxynucleotides into an extending nucleic acid polymer at a rate which is no less than 0.4 times the rate of incorporation of deoxynucleotides. ThermoSequenase™ is exemplary of such an enzyme. Reeve et al., *Nature* 376: 796-797 (1995). Tabor et al. have also described enzymes which have increased processivity and increased levels of
10 incorporation of dideoxynucleotides. (See EP-A1-0 655 506, which is incorporated herein by reference) Roche sells an enzyme under the trademark TAQ-FS which meets these criteria as well.

15 The absolute and relative amounts of nucleotide triphosphates and chain-terminating nucleotide triphosphates may be optimized for the particular enzyme employed. In general, however, the nucleotide triphosphates will be included at in the reaction mixture at concentrations of from 250 μ M to 1.5 mM, and the chain-terminating nucleotide triphosphate will be included at a level of from 0.5 μ M to 30 μ M to produce compositions in which the mole ratio of the chain terminating nucleotide triphosphate to the corresponding nucleotide triphosphate is from 1:50 to 1:1000, preferably from 1:100 to 1:500. This will result in
20 incorporation of a chain-terminating nucleotide triphosphate into from 30 to 100 percent of the extending polymer chains formed during the thermal cycling of the reaction mixture.

25 The method of the invention is suitably practiced using a kit which provides the appropriate reagents in conveniently packaged form. To reduce the number of sample preparation steps, and thus to reduce the risk of erroneous results, such a kit will suitably include at least one pre-prepared mixture comprising all four nucleotide triphosphates and at least one chain terminating nucleotide triphosphate, where the mole ratio of chain terminating

nucleotide to the corresponding deoxynucleotide triphosphate is from 1:50 to 1:1000, preferably 1:100 to 1:500.

The invention will now be further described by way of the following non-limiting examples.

EXAMPLE 1

The presence of the sexually transmitted disease pathogen *Chlamydia trachomatis* in a patient sample is detected according to the method of the invention as follows.

Urine samples from patients suspected of carrying a sexually transmitted disease pathogen are prepared for sequence-based diagnosis as follows. 100 ul of first void urine are deposited in a sterile microcentrifuge tube. The tube is centrifuged at 12,000 x g for 20 min; the supernatant is removed. 100 ul of Lysis Solution (Proteinase K @ 100 g/ml; 1% Tween 20) is added to the bacterial pellet and incubated 1 h at 55°C, or 18 h at room temperature. After a final incubation at 95°C for 10 minutes, 200 ul of GeneClean II glass milk is added, according to the manufacturer's instructions. (Bio 101, Inc) DNA is eluted in 10 ul of double distilled H₂O. (A lysis solution control may be prepared if desired, by adding the lysis solution to a sterile tube (a tube without any urine pellet), and treating this tube like the others.)

The sample natural abundance DNA is then treated according to the method of the invention with a pair of primers and reagents to identify the sequence of a *C. trachomatis* gene present in the sample, if any. A suitable *C. trachomatis* specific target for sequencing is the cryptic plasmid. Primers that may be used are

<u>Name</u>	<u>Sequence</u>	
KL1:	TCCGGAGCGA GTTACGAAGA	[SEQ ID NO: 1]
KL2:	ATTCAATGCC CGGGATTGGT	[SEQ ID NO: 2]

These sequencing primers were employed previously for PCR amplification reactions, but not sequencing (Mahony et al., "Confirmatory polymerase chain reaction testing for

Chlamydia trachomatis in first void urine from asymptomatic and symptomatic men" *J. Clin Microbiol.* 30:2241-2245 (1992)).

5 Either primer may be labeled at the 5'-end with a detectable label such as a Cy5.5 fluorophore. If both primers are labeled, they should be distinguishable. Labels are selected on the basis of the instrument employed for detection. Labeling reactions are performed according to methods well known in the art, such as amidite labeling or dye-ester condensation.

10 The sequencing reaction mixture is prepared by combining 2.5 ul of the prepared DNA sample, 0.67 ul of 10 uM primer KL1 (labeled with Cy5.5), 0.45 ul of KL2 primer at 10 uM, 2 ul of THERMOSEQUENASE reaction buffer (250 mM Tris-HCl pH 9.0 @ 25°C, 39 mM MgCl₂), 2 ul of THERMOSEQUENASE enzyme (Amersham Life Sciences) diluted 1/10 in the dilution buffer provided with the enzyme and 5.38 ul of double distilled H₂O. The final volume is 13 ul.

15 3 ul of the sequencing reaction mixture is placed in each of 4 clean tubes and covered with one drop of mineral oil (Sigma Chemical Co., Cat # M-5904). The tube is placed in a PTC-100 thermal cycler (M.J. Research, Maine) and heated for 3 min at 94°C, then cooled to 85°C. One of the following termination mixtures are then added to each of the 4 tubes:

3 ul of dNTP:ddATP (1 mM each dNTP, 3.3 uM ddATP) in tube A.

3 ul of dNTP:ddCTP (1 mM each dNTP, 3.3 uM ddCTP) in tube C.

20 3 ul of dNTP:ddGTP (1 mM each dNTP, 3.3 uM ddGTP) in tube G.

3 ul of dNTP:ddTTP (1 mM each dNTP, 3.3 uM ddTTP) in tube T.

The dNTP:ddNTP mixes are preferably heated to 85°C when added to the tube. The reaction mixture is mixed well and it is subjected to the following thermal cycling regime for 55 cycles:

25 94°C/30 sec.

60°C/30 sec.

70°C/1 min.

After the last cycle, the tubes are kept at 70°C for 2 min, then cooled to 4°C until ready for loading. To view the reaction products, 6 ul of loading buffer (dye/stop solution) is added to each tube. The aqueous phase (the bottom phase disposed under the oil layer) is removed and put it in another tube. The sample is heated to 75°C for 3 min, and put on ice. 2 ul of each sample is loaded in each well of a MicroGene Blaster automated DNA sequencer (Visible Genetics Inc., Toronto, ON). The reaction products are electrophoretically separated and detected. The data is analyzed using GeneObjects software (Visible Genetics Inc., Toronto, ON) to base-call (i.e. determine the DNA sequence) of the samples. The base-called sequence is compared to the known *C. trachomatis* sequence to confirm diagnosis. Results are reported to the patient file.

EXAMPLE 2

The method of the invention may be employed to identify not only the presence of *C. trachomatis* in a patient sample but also the strain identity. Health care workers currently seek to distinguish among *Chlamydia trachomatis* strains to determine the molecular epidemiologic association of a range of diseases with infecting genotype (See Dean, D. et al "Major Outer Membrane Protein Variants of *Chlamydia trachomatis* Are Associated with Severe Upper Genital Tract Infections and Histopathology in San Francisco." J. Infect. Dis. 172:1013-22 (1995)).

A suitable strain specific target for *C. trachomatis* is the omp1 (outer membrane protein) gene which has at least 4 variable sequence ("VS") domains that may be used to distinguish among the 15 known genotypes of *C. trachomatis* (Yuan, Y et al. "Nucleotide and Deduced Amino Acid Sequences for the Four Variable Domains of the Major Outer Membrane Proteins of the 15 *Chlamydia trachomatis* Serovars" Infect. Immun. 57 1040-1049 (1989)).

Strain identification is achieved using the method of Example 1 with the following modifications. First of all, because of the length of the VS domains, separate reactions are

performed to obtain sequence from VS1/VS2 and VS3/VS4. The following oligonucleotide primers may be employed:

For VS1/VS2:

Name	Sequence	
MF21	CCGACCGCGT CTTGAAAACA GATGT	[SEQ. ID NO. 3]
MB22	CACCCACATT CCCAGAGAGC T	[SEQ. ID NO. 4]

For VS3/VS4

Name	Sequence	
MVF3	CGTGCAGCTT TGTGGGAATG T	[SEQ. ID NO. 5]
MB4	CTAGATTTCA TCTTGTTCAA TTGC	[SEQ. ID NO. 6]

These sequencing primers were employed previously for PCR amplification reactions, but not sequencing. Mahoney et al., *supra*.

These oligonucleotide primers are used in separate reactions in place of KL1 and KL2 in Example 1. The sample preparation and sequencing reactions are performed as in Example 1. The reaction products are electrophoretically separated and detected on a MicroGene Blaster automated DNA sequencing apparatus (Visible Genetics Inc., Toronto, ON). The data is analyzed using GeneObjects software to base-call the samples and to compare the data to the known varieties of *C. trachomatis*. Pure populations generally give unambiguous sequence data. Where heterozygous mixed populations are detected, a circumstance thought to occur in 1-3% of clinical *C. trachomatis* samples, the software identifies the strains which could be combined to result in the particular heterozygote sample detected.

EXAMPLE 3

Strain-specific *C. trachomatis* identification over the VS1/VS2 domain can be achieved according to the method in Example 1, by using the following degenerate primers sets:

Forward

OMP291: AGCATGCGTR TKGGTTACTA YGG [SEQ ID NO. 7]
(labeled with Cy5.5). Base 175 to 197 of the ORF of the omp1 gene of *C. trachomatis*.

Forward

OMP314A: TGACTTTGTT TTCGACCGYG TTTT [SEQ ID NO. 8]
(labeled with Cy5.5). Base 198 to 221 of the ORF of the omp1 gene of *C. trachomatis*.

Reverse

OMP722: CTAAAGTYGC RCATCCACAT TCC [SEQ ID NO. 9]
Base 637 to 615 of the ORF of the omp1 (in serovar K) gene of *C. trachomatis*. The primer may not have the EXACT SAME sequence as in serovar K.

Reverse

OMP711: CATCCACATT CCCASARAGC TGC [SEQ ID NO. 10]
Base 626 to 604 of the ORF of the omp1 (in serovar K) gene of *C. trachomatis*. The primer may not have the exact same sequence as in serovar K.

These primers sets are preferably used in the following combinations:

(1) OMP291-OMP722, sequencing a 455 to 463-bp (depending on the serotype) fragment of the omp1 gene of *C. trachomatis*; or

(2) OMP314A-OMP711, sequencing a 421 to 430-bp (depending on the serotype) fragment of the omp1 gene of *C. trachomatis*.

EXAMPLE 4

5 The method as exemplified in Examples 1, 2 and 3 may be further improved by employing different labels, preferably fluorescent labels, on the different primers for use in a multi-dye sequencer. This method takes advantage of the fact that a given termination mixture containing, for example, ddATP will give chain termination products for the A nucleotide in both directions. The different primer labels means that one reaction mixture loaded in a single lane of an automated DNA sequencing apparatus designed to detect the two labels (a "multi-dye sequencer") will identify the A nucleotide of both sense and antisense strands. Separate reactions are performed for the other 3 nucleotides. Using only 4 lanes of an electrophoresis gel, and 4 reaction mixtures, the DNA sequences of both the sense and anti-sense strands can be obtained. This information allows the operator to resolve any ambiguities that may be present.

10 Use of two different labels lends itself to a further improvement. As noted above, in a reaction according to the invention, the results of the ddATP reaction will give chain termination products for the A nucleotide in both directions. Since the A nucleotide in one direction corresponds to the T nucleotide in the other, a single reaction can provide the location of two bases. A second termination reaction with, for example, ddCTP will then obtain the positions of the other two nucleotides, C and G. Thus only two lanes of an electrophoresis gel and 2 reaction mixtures are required to identify the location of all 4 bases of the sequence.

15 A suitable multi-dye sequencer for use with this aspect of the invention, is the Applied Biosystems 377 Prism automated DNA sequencer (Applied Biosystems Inc., Foster City, CA). The fluorescent labels are selected to be detectable on the 377 instrument. Instead of the dye-terminator chemistry suggested in the Applied Biosystems product literature,

however, the fluorescent labels must be conjugated to the 5' end of the primer molecules. The samples are electrophoresed, detected and the detected data is recorded.

Sophisticated software such as GeneObjects software (Visible Genetics Inc, Toronto, CA) may be used to assist in evaluation of the results. This software may employ the methods of commonly assigned US Patent No. 5,853,979, US Patent Application No. 08/670,534 and International Patent Application No. PCT/US96/11130, published as WO97/02488, all of which are incorporated herein by reference. In one of the methods, the single nucleotide data tracks are evaluated and nucleotides are positioned relative to the known (or standard) DNA sequence expected from the sample. When data tracks are generated for each of the four nucleotides, the full DNA sequence of the sample may be base-called. The base-called sequence is then compared to the library of known sequences to determine which *C. trachomatis* strain or strains are present in the sample.

EXAMPLE 5

The sequence of both the sense strand and antisense strand of a *C. trachomatis* cryptic plasmid gene may be obtained in a one step reaction using the primers:

Name	Sequence	
KL1:	TCCGGAGCGA GTTACGAAGA	[SEQ ID NO. 1]
CT1590:	ATGCCCGGGA TTGGTTGATC	[SEQ ID NO. 11]

Combine the following materials and mix well:

	Concentration	Amount
Patient Sample DNA		11.25 ul
KL1*Cy5.5 Primer	10 uM	3 ul
CT1590*Fluoresceine Primer	10 uM	2 ul
Enzyme Diluent (Amersham plc)		8 ul
ThermoSequenase Enzyme	32 U/ul	0.9 ul

double distilled H₂O

24.2 ul

Take 11 ul of the mixture and add 2 ul of 13X buffer [Tris-HCl 260 mM pH 8.3, MgCl₂ 39 mM] (final concentration 20 mM Tris-HCl pH 8.3, 3 mM MgCl₂). Mix well and place 3 ul into each of 4 tubes. Heat tube to 94°C for 5 mins then reduce temperature to 85°C. Add and mix 3 ul of an 85 C dNTP/ddNTP solution consisting of 0.75 mM each dNTP and 2.5 uM of a chain terminating nucleotide triphosphate (ddNTP) (use a different ddNTP in each of the 4 tubes).

Treat the mixture to 60 cycles of the following thermal cycling reactions: 94°C for 10 sec, 62°C for 15 sec, 70°C for 1 min. Upon completion, treat the mixture for a final 5 min at 70 C and then store at 4°C until ready for loading. For viewing the reaction products, add an equal volume of stop/loading solution (95% formamide plus a colored dye). Take 1.5 ul and load in a single lane of a MicroGene Blaster automated DNA sequencer (Visible Genetics Inc., Toronto). Load the remaining mixture (@ 10.5 ul) in a single lane of an ALF Automated Sequencer (Pharmacia LKB, Uppsala, Sweden). The reaction products from the Cy5.5 labeled primer are detected on the MicroGene Blaster using GeneObjects Software. The reaction products from the fluorescein labeled primer are detected on the ALF Automated Sequencer using GeneObjects Software. The base-calling results of the Cy5.5 labeled primer were compared to the known sequence of the gene by the GeneLibrarian component of GeneObjects.

EXAMPLE 6

As described in U.S. Patent No. 5,834,189, not all 4 nucleotides of *C. trachomatis*, or any polymorphic or multiple allelic locus of any gene or organism necessarily need to be determined in order to ascertain which allele or variant is present. In many cases, positioning less than four nucleotides may be sufficient to determine with certainty which allele is present.

The method of Examples 1- 4 may be modified to obtain single nucleotide data tracks (or fragment patterns) by performing only one of the termination reactions at a time.

In the case of detection and serotyping of *C. trachomatis*, the evaluation of the A track alone over the first 100 nucleotides of the *omp1* gene, aligning to nucleotides 249-349 of the serovars C and K, can distinguish the serovars. Appendix II is a text file representation of the *omp1* gene in each of the serovars. The sequences are all aligned to the last (3') nucleotide of the detectably labeled primer omp314A. (Appendix II shows sequences starting 29 bp downstream of the 3'-nucleotide.) This illustration differs from a traditional "consensus" sequence illustrations in that all missing bases (usually represented by N's or raised dashes) are deleted. The A's are illustrated in the order and positions in which they would be expected to appear after a sequencing reaction and upon detection by an automated DNA electrophoresis apparatus.

If, in another microorganism, the A lane (or other preferred first lane) were not sufficient to distinguish all types, a second reaction for the C, G or T nucleotide could be performed to further define the qualitative nature of any target microorganism present in the sample. Because the sequences of the types are previously known, the operator can determine which of the nucleotides provide the greatest information and will analyze those nucleotides first.

EXAMPLE 7

The presence of and strain identity of *C. trachomatis* in a patient sample may be determined according to the methods of the previous examples by substituting the following primer pairs. These primers are used to determine the sequence of the *omp1* gene (publicly available at DNASIS Accession No. X62921).

Forward Primer (5' Primer) labeled with a detectable label such as Cy5.5:

Primer OMP312: GGAGACTTTG TTTTCGACCG

[SEQ ID NO 12]

Position 312-331 of X62921

and one of the following Reverse Primers (3' Primer) (optionally labeled with a detectable label different from the 5' primer):

Primer OMP708: CATTCCCACA AAGCTGCGCG [SEQ ID NO 13]

Position 727-708 of X62921

Primer OMP706: TTCCCACAAA GCTGCGCGAG [SEQ ID NO 14]

Position 725-706 of X62921

Primer OMP704: CCCACAAAGC TGCGCGAGCG [SEQ ID NO 15]

Position 723-704 of X62921

The following combination can be used to obtain DNA sequence over the following maximum lengths:

OMP312-OMP708: 416-nt region of omp1

OMP312-OMP706: 414-nt region of omp1

OMP312-OMP704: 412-nt region of omp1

EXAMPLE 8

The presence of and strain identity of *C. trachomatis* in a patient sample may be determined according to the method of previous examples, using *C. trachomatis* ribosomal DNA (rDNA) specific primers such as

CT220 ACCTTTCGGT TGAGGGAGAG TCTA [SEQ ID NO 16]

and

CT447 GGACCAATTC TTATTCCCAA GCGA [SEQ ID NO 17]

Haydock et al., Chap 1.10 in Persing et al., *supra*.

EXAMPLE 9

The sequence of both the sense strand and antisense strand of the protease gene of HIV-1 integrated into natural abundance DNA of lymphocytes may be obtained in a one step reaction as follows.

5 Natural abundance DNA is prepared from the patient blood lymphocyte sample according to a standard method such as a standard salting-out procedure (as provided by the Puregene DNA Isolation Kit, Gentra Systems, Inc., Minneapolis) or by detergent and proteinase K treatment (Current Protocols in Molecular Biology, Eds. Ausubel, F.M. et al, (John Wiley & Sons; 1995)).

10 Combine the following materials and mix well:

	Concentration	Amount
Patient Sample DNA		11.25 ul
PR211F*Cy5.5 Primer	10 uM	3 ul
or		
PR281*Cy5.5 Primer	10 uM	3 ul
PR526*Fluorescein Primer	10 uM	2 ul
Enzyme Diluent (Amersham plc)		8 ul
THERMOSEQUENASE Enzyme	32 U/ul	0.9 ul
double distilled H2O		24.2 ul

20 The primers have the following sequences:

Name Sequence

Choice of Forward Primers

PR211F ATCACTCTTT GGCAACGACC [SEQ ID No. 18]

25 (FORWARD), BASE 6 TO 25 OF THE PROTEASE GENE

or

PR281 CAGGAGCAGA TGATACAGTA TTAG [SEQ ID No. 19]

(FORWARD), BASE 76 TO 99 OF THE PROTEASE GENE

Reverse Primer

PR526: CCATTCCTGG CTTTAATTTT ACTGG

[SEQ ID No. 20]

5 (REVERSE), BASES 321 TO 345 OF THE PROTEASE GENE

PR211F-PR526 creates a sequencing fragment of maximum size 340 bp.

PR281-PR526 creates a sequencing fragment of maximum size 270 bp. Both regions contain the sequence of the various codons where mutations are involved in protease inhibitor resistance (Codons 46, 48, 54, 63 82 84 and 90).

10 Take 11 ul of the mixture and add 2 ul of 13X buffer [Tris-HCl 260 mM pH 8.3, MgCl₂ 39 mM] (final concentration 20 mM Tris-HCl pH 8.3, 3 mM MgCl₂). Mix well and place 3 ul into each of 4 tubes. Heat tube to 94 C for 5 mins then reduce temperature to 85 C. Add and mix 3 ul of an 85 C dNTP/ddNTP solution consisting of 0.75 mM each dNTP and 2.5 uM of a chain terminating nucleotide triphosphate (ddNTP) (use a different ddNTP in each of the 4
15 tubes).

20 Treat the mixture to 60 cycles of the following thermal cycling reactions: 94 C for 10 sec, 62 C for 15 sec, 70 C for 1 min. Upon completion, treat the mixture for a final 5 min at 70 C and then store at 4 C until ready for loading. For viewing the reaction products, add an equal volume of stop/loading solution (95% formamide plus a coloured dye). Take 1.5 ul and load in a single lane of a MicroGene Blaster automated DNA sequencer (Visible Genetics Inc., Toronto). Load the remaining mixture (@ 10.5 ul) in a single lane of an ALF Automated Sequencer (Pharmacia LKB, Uppsala, Sweden). The reaction products from the Cy5.5 labelled primer are detected on the MicroGene Blaster using GeneObjects Software. The
25 reaction products from the fluorescein labeled primer are detected on the ALF Automated Sequencer using GeneObjects Software. The base-called results from each primer were compared to the known sequences of HIV-1 by GeneLibrarian (a component of GeneObjects (Visible Genetics Inc, Toronto).

EXAMPLE 10

The presence and type of human papilloma virus (HPV) present in a patient sample can be determined according to the method of the invention by following the protocol in Example 1 with the following modifications.

5 Patient sample DNA is extracted from 250 ul urine specimens using GeneClean II (Bio 101, Inc.). The sample is then treated as described previously but employing the degenerate primer pair:

Forward Primer: MY11

10 GCMCAGGGWC ATAAYAATGG [SEQ ID No. 21]

Reverse Primer: MY09

CGTCCMAARG GAWACTGATC [SEQ ID No. 22]

15 The reactions are performed as before, using ThermoSequenase enzyme or the like. Reaction products are detected on an automated electrophoresis/detection device such as the MicroGene Blaster. The sequence is analyzed and compared to the known varieties of HPV to identify the type. The result is reported to the patient file.

20 Although the preferred embodiments of the invention has been described above in some detail, it should be appreciated that a variety of embodiments will be readily apparent to one skilled in the art. The description of the invention is not intended to be limiting to this invention, but is merely illustrative of the preferred embodiments.

25

APPENDIX I

Suitable Sequencing Primer Pairs for Identification and Sub-Typing of Infectious Pathogens

cf. Diagnostic Molecular Microbiology (Eds. Persing et al.) (1993; American Society for
5 Microbiology; Washington D.C.)

Bacterial Pathogens Universal (16S rDNA) Typing Primers

Pathogen Name: Universal Bacterial Identification

10 Gene: 16s rDNA

Forward Primer: 91E

TCAAAGAAT TGACGGGGGC [SEQ ID No. 23]

Site of Specific Hybridization: nt 911-930

Reverse Primer:13B

15 AGGCCCGGGA ACGTATTCAC [SEQ ID No. 24]

Site of Specific Hybridization: nt 1390-1371

Maximum fragment size: 475 nt

Pathogen Name: Universal Bacterial Identification

20 Gene: 16s rDNA

Forward Primer: 515FPL

TGCCAGCAGC CGCGGTAA [SEQ ID No. 25]

Site of Specific Hybridization: nt 515-533

Reverse Primer:806R

25 GGACTACCAG GGTATCTAAT [SEQ ID No. 26]

Site of Specific Hybridization: nt 806-787

Maximum fragment size: 328 nt

Pathogen Name: Universal Bacterial Identification

Gene: 16s rDNA

Forward Primer: 11E

GAGGAAGGTG GGGATGACGT [SEQ ID No. 27]

5 Site of Specific Hybridization: nt 1175-1194

Reverse Primer: 13B

AGGCCCGGGA ACGTATTAC [SEQ ID No. 28]

Site of Specific Hybridization: nt 1390-1371

Maximum fragment size: 233 nt

10

Pathogen Name: Eubacterial Typing (Broad range of eubacteria)

Gene: 16S rDNA

Forward Primer :285

GAGAGTTTGA TCCTGGCTCA G [SEQ ID No. 29]

15

Site of Specific Hybridization: nt 9-30

Reverse Primer: 244

CCCACTGCTG CCTCCCGTAG [SEQ ID No. 30]

Site of Specific Hybridization: nt 341-361

Maximum fragment size: 352 bp

20

Bacteria

Pathogen Name: Mycobacteria Typing (M. tuberculosis complex)

Gene: 16S rDNA

Forward Primer:285

25

GAGAGTTTGA TCCTGGCTCA G [SEQ ID No. 31]

Site of Specific Hybridization: nt 9-30

Reverse Primer:259

TTTCACGAAC AACGCGACAA

[SEQ ID No. 32]

Site of Specific Hybridization: nt 590-609

Maximum fragment size: 600 bp

5 Pathogen Name: Mycobacterium tuberculosis

Gene: IS6110

Forward Primer:T5

CTCGTCCAGC GCCGCTTCGG

[SEQ ID No. 33]

Site of Specific Hybridization: nt 758-788

Reverse Primer:T4

CCTGCGAGCG TAGGCGTCGG

[SEQ ID No. 34]

Site of Specific Hybridization: nt 881-862

Maximum fragment size: 123 bp

15 Pathogen Name: Rickettsia rickettsii (Rocky Mountain spotted fever)

Gene: 17 K Da Ag Gene

Forward Primer:TZ15

TTCTCAATTC GGTAAGGC

[SEQ ID No. 35]

Site of Specific Hybridization: nt 191-209

20 Reverse Primer :TZ16

ATATTGACCA GTGCTATTTC

[SEQ ID No. 36]

Site of Specific Hybridization: nt 437-419

Maximum fragment size: 247 bp

25 Pathogen Name: Ehrlichia chaffeensis

Gene: 16s rDNA

Forward Primer: HE1

CAATTGCTTA TAACCTTTTG GTTATAAAT

[SEQ ID No. 37]

Site of Specific Hybridization: nt 49-77

Reverse Primer:HE3

TATAGGTACC GTCATTATCT TCCCTAT

[SEQ ID No. 38]

5 Site of Specific Hybridization: nt 438-412

Maximum fragment size: 390 bp

Pathogen Name: *Borrelia burgdorferi* (Lyme disease)

Gene: Outer Surface Protein A

10 Forward Primer:OSPA149

TTATGAAAAA ATATTTATTG GGAAT

[SEQ ID No. 39]

Site of Specific Hybridization: nt 1

Reverse Primer: OSPA319

CTTTAAGCTC AAGCTTGTCT ACTGT

[SEQ ID No. 40]

15 Site of Specific Hybridization: nt 193

Maximum fragment size: 193 bp

Pathogen Name: *Borrelia burgdorferi* (Lyme disease)

Gene: Outer Surface Protein A

20 Forward Primer:OSPA4

CTGCAGCTTG GAATTCAGGC ACTTC

[SEQ ID No. 41]

Site of Specific Hybridization: nt 638

Reverse Primer : OSPA2

GTTTTGTAAT TTCAACTGCT GACC

[SEQ ID No. 42]

25 Site of Specific Hybridization: nt 793

Maximum fragment size: 156 bp

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Pathogen Name: *Borrelia burgdorferi* (Lyme disease)

Gene: 16s rDNA

Forward Primer:DD06

ATCTGTTACC AGCATGTAAT

[SEQ ID No. 43]

Site of Specific Hybridization: nt 1105

Reverse Primer:DD02

CCCTCACTAA ACATACCT

[SEQ ID No. 44]

Site of Specific Hybridization: nt 1472

Maximum fragment size: 368 bp

Pathogen Name: *Borrelia burgdorferi* (Lyme disease)

Gene: Flagellin

Forward Primer:FLA1

GATGATGCTG CTGGCATGGG AGTTTCTGG

[SEQ ID No. 45]

Site of Specific Hybridization: nt 121

Reverse Primer: FLA3

CTGTCTGCAT CTGAATATGT GCCGTTACCT G

[SEQ ID No. 46]

Site of Specific Hybridization: nt 320

Maximum fragment size: bp

Pathogen Name: *Yersinia pestis* (the bubonic plague)

Gene: 9.5 kb pesticin plasmid

Forward Primer: Yp1

ATCTTACTTT CCGTGAGAAG

[SEQ ID No. 47]

Site of Specific Hybridization: nt 971-990

Reverse Primer: Yp2

CTTGGATGTT GAGCTTCCTA

[SEQ ID No. 48]

Site of Specific Hybridization: nt 1450-1431

Maximum fragment size: 478 bp

Pathogen Name: *Treponema pallidum* (venereal syphilis)

5 Gene: 47-kDA gene

Forward Primer: 47-3

TTGTGGTAGA CACGGTGGGT AC

[SEQ ID No. 49]

Site of Specific Hybridization: nt 692 - 713

Reverse Primer: 47-4

10 TGATCGCTGA CAAGCTTAGG CT

[SEQ ID No. 50]

Site of Specific Hybridization: nt 1187-1166

Maximum fragment size: 496 bp

Pathogen Name: *Treponema pallidum* (venereal syphilis)

15 Gene: 16S rDNA

Forward Primer: Tpr3

CTCAGAGATG AGCCTGCGAC CATT

[SEQ ID No. 51]

Site of Specific Hybridization: nt 230

Reverse Primer: TPr4

20 GCATTCCCTC CCGTCCTCAT TCTTC

[SEQ ID No. 52]

Site of Specific Hybridization: nt 480

Maximum fragment size: 251 bp

25 Pathogen Name: *Chlamydia trachomatis* (infection of mucosal surfaces)

Gene: MOMP

Forward Primer: CT.0005

GATAGCGAGC ACAAAGAGAG CTAA

[SEQ ID No. 53]

Site of Specific Hybridization: nt 67

Reverse Primer: CT.06

TTCACATCTG TTTGCAAAAC ACGGTCGAAA ACAAAG

[SEQ ID No. 54]

Site of Specific Hybridization: nt 347

Maximum fragment size: 281 bp

Pathogen Name: Chlamydia pneumoniae (respiratory disease)

Gene: 474bp PST fragment

Forward Primer: HL-1

GTTGTTCATG AAGGCCTACT

[SEQ ID No. 55]

Site of Specific Hybridization: nt 30-49

Reverse Primer: HR-1

TGCATAACCT ACGGTGTGTT

[SEQ ID No. 56]

Site of Specific Hybridization: nt 467-448

Maximum fragment size: 438 bp

Pathogen Name: Mycoplasma pneumoniae (respiratory disease)

Gene: genomic

Forward Primer: MP5-1

GAAGCTTATG GTACAGGTTG G

[SEQ ID No. 57]

Reverse Primer: MP5-2

ATTACCATCC TTGTTGTAAG

[SEQ ID No. 58]

Maximum fragment size: 144 bp

Pathogen Name: Mycoplasma speciation (Universal Primers for 8 most common
Mycoplasma species)

Gene: 16S rDNA

Forward Primer: Primer A

GGCGAATGGG TGAGTAACAC G [SEQ ID No. 59]

Site of Specific Hybridization: nt 87

5 Reverse Primer: Primer B

CGGATAACGC TTGCGACCTA TG [SEQ ID No. 60]

Site of Specific Hybridization: nt 550

Maximum fragment size: 464 bp

10 Pathogen Name: Legionella pneumophila (wound infection, respiratory disease)

Gene:

Forward Primer: LEG1

GCTATGAGGA ATCTCGCTG [SEQ ID No. 61]

Reverse Primer: LEG2

15 CTGGCTTCTT CCAGCTTCA [SEQ ID No. 62]

Maximum fragment size: 800 bp

Pathogen Name: Legionella dumoffii (wound infection, respiratory disease)

Gene:

20 Forward Primer: LDBKS1

ATACACGTGG TGGAGGTAC [SEQ ID No. 63]

Reverse Primer: LDBKS2

GCGGGCAATA TCTTGCATC [SEQ ID No. 64]

Maximum fragment size: 1000 bp

25

Pathogen Name: Mycoplasma fermentans

Gene: IS-like element

Forward Primer:RW005

GGTTATTCGA TTTCTAAATC GCCT

[SEQ ID No. 65]

Site of Specific Hybridization: nt 1116

Reverse Primer:RW004

5 GGACTATTGT CTAAACAATT TCCC

[SEQ ID No. 66]

Site of Specific Hybridization: nt 1321

Maximum fragment size: 206 nt

Pathogen Name: Ehrlichia

Gene: 16S rDNA

Forward Primer: 8F

AGTTTGATCA TGGCTCAG

[SEQ ID No. 67]

Site of Specific Hybridization: nt 32

Reverse Primer:GA1UR

15 GAGTTTGCCG GGA CTTCTTC T

[SEQ ID No. 68]

Site of Specific Hybridization: nt (about 400)

Maximum fragment size: (about 400 nt)

20 Viruses

Human Immunodeficiency Virus Type 1 (HIV-1)

Gene: gag

Forward Primer:SK462

25 AGTTGGAGGA CATCAAGCAG CCATGCAAAT

[SEQ ID No. 69]

Site of Specific Hybridization:1366-1395: nt

Reverse Primer:SK431

TGCTATGTCA GTTCCCCTTG GTTCTCT

[SEQ ID No. 70]

Site of Specific Hybridization: nt 1507-1481

Maximum fragment size: 142 nt

5

Human T-Cell Lymphotropic Virus Type 1 (HTLV-1)

Gene: POL

Forward Primer: POL1

CCCGGGCCCC CTGACTTGTC

[SEQ ID No. 71]

Site of Specific Hybridization: nt 2802-2821

Reverse Primer: POL3

GCTTTCCTG TCCCACAGCAG

[SEQ ID No. 72]

Site of Specific Hybridization: nt 2916-2936

Maximum fragment size: 237 nt

Hepatitis B Virus (HBV)

Gene: surface antigen

Forward Primer: Primer 1

CAAGGTATGT TGCCCGTTTG

[SEQ ID No. 73]

Site of Specific Hybridization: nt 329-348

Reverse Primer: Primer 2

AAAGCCCTGC GAACCACTGA

[SEQ ID No. 74]

Site of Specific Hybridization: nt 587-568

Maximum fragment size: 259 nt

25

Hepatitis C Virus (HCV)

Gene: 5'UT

Forward Primer:5PUT c1-a

CCCAACACTA CTCGGCTAG

[SEQ ID No. 75]

Site of Specific Hybridization: nt -74--92

Reverse Primer:5PUT 1-s

5 AACTACTGTC TTCACGCAGA AAGC

[SEQ ID No. 76]

Site of Specific Hybridization: nt -266--289

Maximum fragment size: 216 nt

Herpes simplex virus (HSV)

10 Gene: DNA polymerase gene

Forward Primer: HSV-3

TACATCGGCG TCATCTGCGG GG

[SEQ ID No. 77]

Site of Specific Hybridization: nt 2821-2842

Reverse Primer: HSV-4

15 CAGTTCGGCG GTGAGGACAA AG

[SEQ ID No. 78]

Site of Specific Hybridization: nt 3090-3111

Maximum fragment size: 290 nt

Herpesvirus 6

20 Gene:

Forward Primer:H6-6

AAGCTTGACAC AATGCCAAAA AACAG

[SEQ ID No. 79]

Reverse Primer:H6-7

CTCGAGTATG CCGAGACCCC TAATC

[SEQ ID No. 80]

25 Maximum fragment size: 223 nt

Herpesvirus 7

Gene:

Forward Primer:HV7

TATCCCAGCT GTTTTTCATAT AGTAAC

[SEQ ID No. 81]

Reverse Primer: HV8

5 GCCTTGCGGT AGCACTAGAT TTTTGTG

[SEQ ID No. 82]

Maximum fragment size: 186 nt

Epstein-Barr Virus

Gene: EBNA2

10 Forward Primer:E2p1

AAGGATGCCT GGACACAAGA

[SEQ ID No. 83]

Site of Specific Hybridization: nt 1813-1833

Reverse Primer:E2p2

15 TGGTGCTGCT GGTGGTGGCA AT

[SEQ ID No. 84]

Site of Specific Hybridization: nt 2409-2388

Maximum fragment size: 596 nt

Cytomegalovirus (CMV) (member of Herpesviridae)

Gene: CMV IE gene

20 Forward Primer:CMV1

CCTAGTGTGG ATGACCTACG GGCCA

[SEQ ID No. 85]

Site of Specific Hybridization: nt 1234-1258

Reverse Primer:CMV2

25 CAGACACAGT GTCCTCCCGC TCCTC

[SEQ ID No. 86]

Site of Specific Hybridization: nt 1459-1483

Maximum fragment size: 249 nt

Varicella-Zoster Virus (VZV) (for Chicken Pox)

Gene: unique genomic fragment

Forward Primer:VZ7

ATGTCCGTAC AACATCAACT

[SEQ ID No. 87]

5 Site of Specific Hybridization: nt 3377-3396

Reverse Primer:VZ8

CGATTTTCCA AGAGAGACGC

[SEQ ID No. 88]

Site of Specific Hybridization: nt 3643-3624

Maximum fragment size: 267 nt

10

JC Virus (JCV) distinguishing from BK virus and simian virus 40

Gene: T antigen

Forward Primer:P5

AGTCTTTAGG GTCTTCTACC

[SEQ ID No. 89]

15 Site of Specific Hybridization: nt 4255-4274

Reverse Primer:P6

GGTGCCAACC TATGGAACAG

[SEQ ID No. 90]

Site of Specific Hybridization: nt 4427-4408

Maximum fragment size: 172 nt

20

Parvovirus B19

Gene: VP Protein

Forward Primer: Z

GGAACAGACT TAGAGCTTAT TC

[SEQ ID No. 91]

25 Site of Specific Hybridization: nt 2537

Reverse Primer: Y

GCTTGTGTAA GTCTTCACTA G

[SEQ ID No. 92]

Site of Specific Hybridization: nt 2774

Maximum fragment size: 259 nt

Influenza A (Orthomyxoviridae)

5 Gene: hemagglutinin H2

Forward Primer:AH2B

CAATAGCTGG TTTTATAGAA [SEQ ID No. 93]

Site of Specific Hybridization: nt 1077

Reverse Primer:AH2CII

10 TTATCATACA GATTCTTGAC [SEQ ID No. 94]

Site of Specific Hybridization: nt 1425

Maximum fragment size: 349 nt

Influenza B (Orthomyxoviridae)

15 Gene: Matrix Protein

Forward Primer: BMPB

GAAGGCAAAG CAGAACTAGC [SEQ ID No. 95]

Site of Specific Hybridization: nt 79

Reverse Primer: BMPCII

20 TGGCCTTCTG CTATTTCAAA [SEQ ID No. 96]

Site of Specific Hybridization: nt 380

Maximum fragment size: 302 nt

Influenza C (Orthomyxoviridae)

25 Gene: hemagglutinin

Forward Primer:CHAB

GTGCAAACCTG CATCTTGTGG [SEQ ID No. 97]

Site of Specific Hybridization: nt 705

Reverse Primer:CHACII

CTCATTTCTT GATCTCCATG

[SEQ ID No. 98]

Site of Specific Hybridization: nt 1145

5 Maximum fragment size: 441 nt

Rotavirus

Gene: vp7

Forward Primer:A2

10 GGACCAAGAG AAAACGTAGC

[SEQ ID No. 99]

Site of Specific Hybridization: nt 805

Reverse Primer:A4

GGTCACATCA TACAATTCTA ATCTAAG

[SEQ ID No. 100]

Site of Specific Hybridization: nt 1062

15 Maximum fragment size: 257 nt

Human Adenovirus

Gene: Hexon gene

Forward Primer:A2H/pcr 4R

20 ATGACTTTTG AGGTGGATCC CATGGA

[SEQ ID No. 101]

Reverse Primer:A2H/pcr 1

GCCGAGAAGG GCGTGCGCAG GTA

[SEQ ID No. 102]

Maximum fragment size: 134 nt

25 Rubella Virus

Gene: 40S ssRNA

Forward Primer:Ru2

TGCTTTGCCC CATGGGACCT CGAG

[SEQ ID No. 103]

Site of Specific Hybridization: nt 1990-2013

Reverse Primer:Ru3

GGCGAACACG CTCATCACGG T

[SEQ ID No. 104]

5 Site of Specific Hybridization: nt 2310-2290

Maximum fragment size: 321 nt

Human Enteroviruses

Gene: 5'NTR

10 Forward Primer:MD91

CCTCCGGCCC CTGAATGCGG CTAAT

[SEQ ID No. 105]

Site of Specific Hybridization: nt 444-468

Reverse Primer:MD90

ATTGTCACCA TAAGCAGCCA

[SEQ ID No. 106]

15 Site of Specific Hybridization: nt 577-596

Maximum fragment size: 154 nt

Genital Human Papillomavirus (HPV)

Gene: L1 gene

20 Forward Primer:MY11

GCMCAGGGWC ATAAYAATGG

[SEQ ID No. 107]

Site of Specific Hybridization: nt 6582

Reverse Primer:MY09

CGTCCMAARG GAWACTGATC

[SEQ ID No. 108]

25 Site of Specific Hybridization: nt 7033

Maximum fragment size: 450 nt

Hantavirus

Gene: M segment

Forward Primer:Har M 30+

CACTGAATAA GAGGATACAA GAATGG

[SEQ ID No. 109]

Site of Specific Hybridization: nt 30

Reverse Primer:Har M 403-

GGAGGAATAT TACATGTGCC TTT

[SEQ ID No. 110]

Site of Specific Hybridization: nt 403

Maximum fragment size: 374 nt

Fungi

Cryptococcus neoformans (Universal fungal primers)

Gene:

Forward Primer: ITS1

TCCGTAGGTG AACCTGCGA

[SEQ ID No. 111]

Reverse Primer:ITS4

TCCTCCGCTT ATTGATATGC

[SEQ ID No. 112]

Maximum fragment size: 600 nt

Pneumocystis carinii

Gene: 5S rDNA

Forward Primer:5S Sense

AGTTACGGCC ATACCTCAGA

[SEQ ID No. 113]

Reverse Primer:5S Antisense

AAAGCTACAG CACGTCGTAT

[SEQ ID No. 114]

Maximum fragment size: 120 nt

Fungal Pathogens (*Histoplasma capsulatum*, *Blastomyces dermatitidis*, *Coccidioides immitis* *Trichophyton rubrum*)

5 Gene: 18S rDNA

Forward Primer: NS3

GCAAGTCTGG TGCCAGCAGC C

[SEQ ID No. 115]

Site of Specific Hybridization: nt 551

Reverse Primer: RDR116

10 CCGTCAATTC CTTTATGTTT CAGCCTT

[SEQ ID No. 116]

Site of Specific Hybridization: nt 1149

Maximum fragment size: 599 nt

15 Protozoa

Trypanosoma cruzi

Gene: kinetoplast

Forward Primer: S35

20 AAATAATGKA CGGGTGAGAT GCATGA

[SEQ ID No. 117]

Reverse Primer: S36

GGGTTCGATT GGGGTTGGTG T

[SEQ ID No. 118]

Maximum fragment size: 330 nt

25 *Leishmania* species

Gene: kinetoplast

Forward Primer: 13A

GTGGGGGAGG GGCGTTCT

[SEQ ID No. 119]

Reverse Primer:13B

ATTTTACACC AACCCCCAGT T

[SEQ ID No. 120]

Maximum fragment size: 120 nt

5

Plasmodium (genus specific)

Gene: Nuclear small subunit rDNA

Forward Primer: 566R

GGATAACTAC GGAAAAGCTG TAGC

[SEQ ID No. 121]

or Forward Primer: 570R

CGACTTCTCC TTCCTTTAAA AGATAGG

[SEQ ID No. 122]

Reverse Primer:567R

GTTCAAGATT AATAATTGCA ATAATCTATC CC

[SEQ ID No. 123]

Maximum fragment size: about 500 nt

15

Entamoeba histolytica (amoebic dysentery)

Gene: SSU rDNA

Forward Primer:Psp5

GGCCAATTCA TTCAATGAAT TGAG

[SEQ ID No. 124]

Site of Specific Hybridization: nt 200

Reverse Primer:Psp3

CTCAGATCTA GAAACAATGC TTCTC

[SEQ ID No. 125]

Site of Specific Hybridization: nt 1075

Maximum fragment size: 876 nt

25

Babesia microti

Gene: SS rDNA

Forward Primer:Bab1

CTTAGTATAA GCTTTTATAC AGC

[SEQ ID No. 126]

Site of Specific Hybridization: nt 38-60

Reverse Primer:Bab4

5 ATAGGTCAGA AACTTGAATG ATACA

[SEQ ID No. 127]

Site of Specific Hybridization: nt 251-275

Maximum fragment size: 238 nt

Giardia lamblia

Gene: 18S rDNA gene

Forward Primer:JW1

GCGCACCAGG AATGTCTTGT

[SEQ ID No. 128]

Site of Specific Hybridization: nt 1251-1270

Reverse Primer:JW2

15 TCACCTACGG ATACCTTGTT

[SEQ ID No. 129]

Site of Specific Hybridization: nt 1433-1414

Maximum fragment size: 183 nt

Pathogen Name: Cryptosporidium oocyst detection

20 Gene: 18S rDNA

Forward Primer: CP1

CCGAGTTTGA TCCAAAAAGT TACGAA

[SEQ ID No. 130]

Reverse Primer: CP2

TAGCTCCTCA TATGCCTTAT TGAGTA

[SEQ ID No. 131]

25 Maximum fragment size: 452 nt

Pathogen Name: Cyclospora and Eimeria species

Gene: 18S rDNA

Forward Primer: CYC3FE

GGAATTCCTT CCGAGCTTCG CTGCGT [SEQ ID No. 132]

Site of Specific Hybridization: nt 685-704

5 Reverse Primer: CYC4RB

CGGGATCCCG TCTTCAAACC CCCTACTG [SEQ ID No. 133]

Site of Specific Hybridization: nt 978-959

Maximum fragment size: 294 nt

10 Identification of Bacterial Toxin Genes

Pathogen Name: *Vibrio cholerae* 01 containing cholera toxin gene (epidemic cholera)

Gene: CTXA

15 Forward Primer: CTX2

CGGGCAGATT CTAGACCTCC TG [SEQ ID No. 134]

Site of Specific Hybridization: nt 73-94

Reverse Primer: CTX3

CGATGATCTT GGAGCATTCC CAC [SEQ ID No. 135]

20 Site of Specific Hybridization: nt 614-636

Maximum fragment size: 564 bp

Pathogen Name: Enterotoxigenic *Escherichia coli*

Gene: ST1a or ST1b

25 Forward Primer: ST1-1

TTAATAGCAC CCGGTACAAG CAGG [SEQ ID No. 189]

Site of Specific Hybridization: nt 243-266

Reverse Primer: ST1-2

CTTGACTCTT CAAAAGAGAA AATTAC

[SEQ ID No. 136]

Site of Specific Hybridization: nt 127-144

Maximum fragment size: 147 bp

5

Pathogen Name: Enterotoxigenic Escherichia coli

Gene: LT1a or LT1b

Forward Primer: LT1a/b-1

TCTCTATRTG CAYACGGAGC

[SEQ ID No. 137]

Site of Specific Hybridization: nt 46-65

Reverse Primer: LT1-2

CCATACTGAT TGCCGCAAT

[SEQ ID No. 138]

Site of Specific Hybridization: nt 349-367

Maximum fragment size: 322 bp

10

Pathogen Name: Enterotoxigenic Escherichia coli

Gene: SLTII

Forward Primer:SLTII-1

CTTCGGTATC CTATTCCCGG

[SEQ ID No. 139]

Site of Specific Hybridization: nt 288-307

Reverse Primer:SLTII-2

GGATGCATCT CTGGTCATTG

[SEQ ID No. 140]

Site of Specific Hybridization: nt 747-766

Maximum fragment size: 478 bp

15

20

25

Pathogen Name: Shigella species and enteroinvasive E. coli (diarrheal disease)

Gene: Invasion plasmid ial locus

Forward Primer: Sh-1

CTGGATGGTA TGGTGAGG [SEQ ID No. 141]

Reverse Primer: Sh-2

GGAGGCCAAC AATTATTTCC [SEQ ID No. 142]

5 Maximum fragment size: 320 bp

Pathogen Name: *Helicobacter pylori* (formerly *Campylobacter pylori*)

Gene: genomic

Forward Primer: CAM-2

10 TAACAAACCG ATAATGGCGC [SEQ ID No. 143]

Reverse Primer: CAM-4

CATCTTGTTA GAGGGATTGG [SEQ ID No. 144]

Maximum fragment size: 203 bp

15 Pathogen Name: Toxigenic *Clostridium difficile*

Gene: rDNA

Forward Primer: PG-48

CTCTTGAAAC TGGGAGACTT GA [SEQ ID No. 145]

Reverse Primer: B

20 CCGTCAATTC MTTTTRAGTTT [SEQ ID No. 146]

Maximum fragment size: 291 bp

Pathogen Name: Toxigenic *Clostridium difficile*

Gene: Toxin B

25 Forward Primer: YT-17

GGTGGAGCTT CAATTGGAGA G [SEQ ID No. 147]

Reverse Primer: YT-18

GTGTAACCTA CTTTCATAAC ACCAG

[SEQ ID No. 148]

Maximum fragment size: 399 bp

5 Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: sea

Forward Primer:SEA1

TTGGAAACGG TTAAAACGAA

[SEQ ID No. 149]

Site of Specific Hybridization: nt 490-509

10 Reverse Primer:SEA2

GAACCTTCCC ATCAAAAACA

[SEQ ID No. 150]

Site of Specific Hybridization: nt 610-591

Maximum fragment size: 120 bp

15 Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: seb

Forward Primer:SEB1

TCGCATCAAA CTGACAAACG

[SEQ ID No. 151]

Site of Specific Hybridization: nt 634-653

20 Reverse Primer:SEB2

GCAGGTACTC TATAAGTGCC

[SEQ ID No. 152]

Site of Specific Hybridization: nt 1110-1091

Maximum fragment size: 478 bp

25 Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: sec

Forward Primer: SEC1

GACATAAAAG CTAGGAATTT

[SEQ ID No. 153]

Site of Specific Hybridization: nt 676-695

Reverse Primer:SEC2

AAATCGGATT AACATTATCC

[SEQ ID No. 154]

5 Site of Specific Hybridization: nt 932-913

Maximum fragment size: 257 bp

Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: sed

10 Forward Primer:SED1

CTAGTTTGGT AATATCTCCT

[SEQ ID No. 155]

Site of Specific Hybridization: nt 354-373

Reverse Primer:SED2

TAATGCTATA TCTTATAGGG

[SEQ ID No. 156]

15 Site of Specific Hybridization: nt 671-652

Maximum fragment size: 317 bp

Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: see

20 Forward Primer:SEE1

TAGATAAAGT TAAAACAAGC

[SEQ ID No. 157]

Site of Specific Hybridization: nt 491-510

Reverse Primer:SEE2

TAACTTACCG TGGACCCTTC

[SEQ ID No. 158]

25 Site of Specific Hybridization: nt 659-640

Maximum fragment size: 170 bp

Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: tss

Forward Primer:TSST1

ATGGCAGCAT CAGCTTGATA [SEQ ID No. 159]

5 Site of Specific Hybridization: nt 251-270

Reverse Primer:TSST2

TTTCCAATAA CCACCCGTTT [SEQ ID No. 160]

Site of Specific Hybridization: nt 600-581

Maximum fragment size: 350 bp

10 Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: eta

Forward Primer:ETA1

CTAGTGCATT TGTTATTCAA [SEQ ID No. 161]

15 Site of Specific Hybridization: nt 374-393

Reverse Primer:ETA2

TGCATTGACA CCATAGTACT [SEQ ID No. 162]

Site of Specific Hybridization: nt 492-473

Maximum fragment size: 119 bp

20 Pathogen Name: Staphylococcus aureus toxins and virulence factors

Gene: etb

Forward Primer:ETB1

ACGGCTATAT ACATTCAATT [SEQ ID No. 163]

25 Site of Specific Hybridization: nt 51-70

Reverse Primer:ETB2

TCCATCGATA ATATACCTAA [SEQ ID No. 164]

Site of Specific Hybridization: nt 250-231

Maximum fragment size: 200 bp

Pathogen Name: Bacterial meningitis (Haemophilus influenzae, Neisseria meningitidis,
5 Streptococcus pneumonia, S. agalactiae, Listeria monocytogenes, enteric bacteria, or
Mycobacterium tuberculosis)

Gene: 16s rDNA

Forward Primer:RW01

AACTGGAGGA AGGTGGGGAT [SEQ ID No. 165]

Reverse Primer:DG74

AGGAGGTGAT CCAACCGCA [SEQ ID No. 166]

Maximum fragment size: 370 nt

Pathogen Name: Streptococcus pyogenes exotoxins (Streptococcal Toxic Shock Syndrome)

Gene: speC

Forward Primer:F

CCACCTTGAC TATTT [SEQ ID No. 167]

Reverse Primer:R

TTAATTAGGA GGTA [SEQ ID No. 168]

Maximum fragment size: 936 nt

Identification of Anti-Microbial Resistance Loci

25 Pathogen Name: Rifampin Resistance Mutations in Mycobacterium tuberculosis and M.
leprae

Gene: rpoB

Forward Primer:rpoB105

CGTGGAGGCG ATCACACCGC AGACGT [SEQ ID No. 169]

Reverse Primer:rpoB293

AGTGCGACGG GTGCACGTCG CGGACCT [SEQ ID No. 170]

5 Maximum fragment size: 215 nt

Pathogen Name: Human Immunodeficiency Virus Drug Resistance

Gene: HIV Reverse Transcriptase

Forward Primer:A(35)

10 TTGGTTGCAC TTAAATTTT CCCATTAGTC CTATT [SEQ ID No. 171]

Reverse Primer:NE-1(35)

CCTACTAACT TCTGTATGTC ATTGACAGTC CAGCT [SEQ ID No. 172]

Maximum fragment size: 805 nt

15 Pathogen Name: erm Erythromycin Resistance Genes (in S. aureus, E. coli, or Bacillus
sphaericus)

Gene: erm

Forward Primer:E1

GARATIGGII IIGGIAARGG ICA* [SEQ ID No. 173]

20 Reverse Primer:E2

AAYTGRTTYT TIGTRAA* [SEQ ID No. 174]

Maximum fragment size: 530 nt

*I=inosine

25 Pathogen Name: Methicillin-Resistant Staphylococcus

Gene: mecA

Forward Primer:RSM 2647

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PATENT APPLICATION

AAAATCGATG GTAAAGGTTG GC

[SEQ ID No. 175]

Site of Specific Hybridization: nt 1282-1303

Reverse Primer: RSM 2648

AGTTCTGCAG TACCGGATTT GC

[SEQ ID No. 176]

5 Site of Specific Hybridization: nt 1814-1793

Maximum fragment size: 533 nt

Pathogen Name: Penicillinase-Producing *Neisseria gonorrhoeae*

Gene: TEM-1

10 Forward Primer:PPNG-L

AGTTATCTAC ACGACGG

[SEQ ID No. 177]

Reverse Primer:PPNG-R

GGCGTACTAT TCACTCT

[SEQ ID No. 178]

Maximum fragment size: 761 nt

15 Pathogen Name: Aminoglycoside-Modifying Enzymes

Gene: aacC1

Forward Primer:aacC1-1

ACCTACTCCC AACATCAGCC

[SEQ ID No. 179]

20 Reverse Primer:aacC1-2

ATATAGATCT CACTACGCGC

[SEQ ID No. 180]

Maximum fragment size: 169 nt

Pathogen Name: Extended Spectrum of Beta-lactamases

25 Gene: TEM-1

Forward Primer:Lag.Std.3

AGAGAATTAT GCAGTGC

[SEQ ID No. 181]

Site of Specific Hybridization: nt 560

Reverse Primer:Amp. Primer 2

GACAGTTACC AATGCTTAAT CA [SEQ ID No. 182]

Site of Specific Hybridization: nt 1074

5 Maximum fragment size: 514 nt

Pathogen Name: Fluoroquinolone Resistance mutations in Mycobacterium tuberculosis

Gene: gyrA

Forward Primer:GyrA1

10 CAGCTACATC GACTATGCGA [SEQ ID No. 183]

Site of Specific Hybridization: nt 78-97

Reverse Primer:GyrA2

GGGCTTCGGT GTACCTCAT [SEQ ID No. 184]

Site of Specific Hybridization: nt 379-397

15 Maximum fragment size: 320 nt

Pathogen Name: Isoniazid Resistance of Mycobacterium tuberculosis

Gene: katG

Forward Primer:katG904

20 AGCTCGTATG GCACCGGAAC [SEQ ID No. 185]

Site of Specific Hybridization: nt 904

Reverse Primer:katG1523

TTGACCTCCC ACCCGACTTG [SEQ ID No. 186]

Site of Specific Hybridization: nt 1523

25 Maximum fragment size: 620 nt

Pathogen Name: Vancomycin resistant Enterococci

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Gene: vanB

Forward Primer:VanB1

CATCGCCGTC CCCGAATTTC AAA

[SEQ ID No. 187]

Reverse Primer:VanB2

5 GATGCGGAAG ATACCGTGGC T

[SEQ ID No. 188]

Maximum fragment size: 297 nt